



|||||ATGTTAGATAAGGACAAGGCCACATATGACTGTTCACTCATATAAGGGCCAAAGGACTAGTICCA  
 300 310 320 330 340 350 360 370  
 440 450 460 470 480 490 500  
 TGACCAAAATGAGGTTGACCTATCGTCAACTCGTAACTCTAACAGTAACCTCTTATA  
 TGCACCAAAATGAGGTTGACCTATCGTCAACTCGTAACTCTAACAGTAACCTCTTATA  
 380 390 400 410 420 430 440  
 510 520 530 540 550 560 570  
 GAAAGAAATCTGGATCATAATTGACTGCTCATTCAGGTACCCAGAACCTTGGAGATGT  
 |||||GAAAGAAATCTGGATCATAATTGACTGCTCATTCAGGTACCCAGAACCTTGGAGATGT  
 450 460 470 480 490 500 510  
 580 590 600 610 620 630 640  
 ATTTCAGCTAACACTGAGATTCAACTAAGTATGATGACTGTCATGAAGAATCTCAAATATGTA  
 ATTTCAGCTAACACTGAGATTCAACTAAGTATGATGACTGTCATGAAGAATCTCAAATATGTA  
 520 530 540 550 560 570 580  
 650 660 670 680 690 700 710 720  
 CAGAACTGTTACAGTTCTATCGTTGCTTTCAGCTTCTGAAAGCACAATGTAAGGCGCTTTGTG  
 CAGAACTGTTACAGTTCTATCGTTGCTTTCAGCTTCTGAAAGCACAATGTAAGGCGCTTTGTG  
 590 600 610 620 630 640 650  
 730 740 750 760 770 780 790  
 CCCTGAAACTGGAGACATGGAGATGCTGCTCCCTACCTTCAATTAGTATGCAACACTTAAAG  
 CCCTGAAACTGGAGACATGGAGATGCTGCTCCCTACCTTCAATTAGTATGCAACACTTAAAG  
 660 670 680 690 700 710 720 730  
 800 810 820 830 840 850 860  
 ACCCTGAAAGGCCACTTCCTCTGATGGGGCTGACTCTGTAATGTTGTTGTTGTTGTTGTTG  
 ACCCTGAAAGGCCACTTCCTCTGATGGGGCTGACTCTGTAATGTTGTTGTTGTTGTTGTTG  
 740 750 760 770 780 790 800  
 870 880 890 900 910 920 930  
 CCTTAAACACTAAAGGAAAAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG  
 CCTTAAACACTAAAGGAAAAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG  
 810 820 830 840 850 860 870  
 940 950 960 970 980 990 1000  
 AGAGAAAAGAGGCAACAGGCCAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG  
 AGAGAAAAGAGGCAACAGGCCAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG  
 880 890 900 910 920 930 940  
 1010 1020 1030 1040 1050 1060 1070 1080  
 GTGTTAACATTGAGAACAGCTCAGGGGCAAAATCAGTAGGAAAATGGTGGCTTGCTGCAAT  
 GTTAACTACATTGAGAACAGCTCAGGGGCAAAATCAGTAGGAAAATGGTGGCTTGCTGCAAT  
 950 960 970 980 990 X  
 Sequence 9, Application US/09646561

TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY  
 MOLECULES, AND USES THEREOF  
 GENERAL INFORMATION:  
 APPLICANT: IM-1-C1-PCT  
 APPLICANT: Yang, Shumin  
 APPLICANT: Sellins, Karen S.  
 PRIORITY NUMBER: US/09/646,561  
 CURRENT FILING DATE: 2000-09-19  
 PRIORITY NUMBER: 60/078,765

PRIOR FILING DATE: 1998-03-19  
 PRIORITY NUMBER: 09/0062,597  
 PRIOR FILING DATE: 1998-04-17  
 NUMBER OF SEQ ID NOS: 65  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 9  
 LENGTH: 987  
 TYPE: DNA  
 ORGANISM: Canis familiaris  
 Initial Score = 706 Optimized Score = 868 Significance = 0.36  
 Residue Identity = 87% Matches = 875 Mismatches = 112  
 Gaps = 13 Conservative Substitutions = 0  
 GRITCTGTTCTCCCTGGAAATGTCATGAGCTTATACATCTGGCTCTGAGGCTCTGGCTCTGAGCTTCTG  
 10 20 30 40 50 60 X 70  
 AT-GTATCT  
 X  
 80 90 100 110 120 130 140  
 GTGACAGACTATGGACTGACTCAACTCTCCTTGTGATGCCCTCTGCTCTGGCTCTGCTCTGGCTCTG  
 CAGA-TGCACTATGGACTGACTGATAACATTCTCTTGTGACCTCCCTGCTCTGGCTCTGCTCTG  
 10 20 30 40 50 60 70  
 AGAGTCAAGCATTAACTAACAGACTGAGACTGGCATGCTGCAATACATCAACATAGCTGG  
 AGAGTCAAGCATTAACTAACAGACTGAGACTGGCATGCTGCAATACATCAACATAGCTGG  
 150 160 170 180 190 200 210  
 AGAGTCAAGCATTAACTAACAGACTGAGACTGGCATGCTGCAATACATCAACATAGCTGG  
 AGAGTCAAGCATTAACTAACAGACTGAGACTGGCATGCTGCAATACATCAACATAGCTGG  
 80 90 100 110 120 130 140 150  
 220 230 240 250 260 270 280  
 ATAGCTGTGATGTTGGAGGACAGGATAAGGCTGAGACTGGTCTGTATGAGATACTAGAGGAAAGAAC  
 ATGAGTCTGTGATGTTGGAGGACAGGATAAGGCTGAGACTGGTCTGTATGAGATACTAGAGGAAAGAAC  
 220 230 240 250 260 270 280  
 CTCAAATGTCATCTCAAATAAGGGCGTACAGGCTTGTGAGGAAACTGGCTCTGAGACTCCACA  
 CTCAAATGTCATCTCAAATAAGGGCGTACAGGCTTGTGAGGAAACTGGCTCTGAGACTCCACA  
 230 240 250 260 270 280 290  
 290 300 310 320 330 340 350 360  
 ATGTTCACTCAGGAGCAGGACATACTCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTG  
 ATGTTCACTCAGGAGCAGGACATACTCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTG  
 290 300 310 320 330 340 350 360  
 TGACACAAATGAGCTCTGACTCTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTG  
 TGACACAAATGAGCTCTGACTCTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTG  
 300 310 320 330 340 350 360  
 510 520 530 540 550 560 570  
 GAACAGAAATCTGGATCATATAATTGACTCTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTG  
 GAACAGAAATCTGGATCATATAATTGACTCTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTG  
 440 450 460 470 480 490 500 510  
 580 590 600 610 620 630 640  
 ATTTCTGCTAAACCTGAGAACTTCAACTAAAGTATGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTG  
 ATTTCTGCTAAACCTGAGAACTTCAACTAAAGTATGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTG  
 520 530 540 550 560 570 580  
 CAGAACCTGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  
 CAGAACCTGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  
 590 600 610 620 630 640 650

Page 3

4. US-09-303-040-5 (1-1080)  
US-09-646-561-30 Sequence 30, Application US/09646561

Sequence 30, Application US/09646561

GENERAL INFORMATION

APPLICANT: Sim, Ge-Kee

APPLICANT: Yang, Shumin

APPLICANT: Sellins, Karen S.

TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY

PROTBINS, NUCLEIC

CURRENT APPLICATION NUMBER: US/09/646,561

CURRENT FILING DATE: 2000-09-19

PRIOR FILING DATE: 1998-03-19

PRIOR APPLICATION NUMBER: 09/062,597

PRIOR FILING DATE: 1998-04-17

SOFTWARE NUMBER: SEQ ID NO: 65

FILE REFERENCE: IM-1-CI-PCT

SEQ ID NO: 30

LENGTH: 509

TYPE: DNA

ORGANISM: *Felis catus*

FEATURE:

NAME/KEY: CDS

LOCATION: (1) .. (507)

Initial Score = 497 Optimized Score = 501 Significance = -0.40  
Residue Identity = 98% Matches = 502 Mismatches = 7  
Gaps = 1 Conservative Substitutions = 0

GRTTCTGTTCTCGGAAATGTCAGTGCAGCTTACATGCTGGGACTCTGCTGAGCTGTGGATGGCATT  
80 90 100 110 120 130 140  
GTGACAGCACTATGGGACTGACTGACTCACTCTCCCTGTGATGGGCCCTCTCTGTGTTCTCCATGA  
150 160 170 180 190 200 210  
AGAGTCAGCATTTAACAGACTGAGAAGCTCCATGCAATTACCTCAAAACATAGCTGG  
220 230 240 250 260 270 280  
ATGAGCTGGTAGTTTGGCAGGACAGGATAAGCTGGTTCTTATAGATAATTGAGGAAAGAAC  
290 300 310 320 330 340 350 360  
CTCAAATGTTCATCTCAAAATAAGGGCCTGAGGACACTGGGCCNGAGACTCCACA  
370 380 390 400 410 420 430  
ATGTTCAAGGACAGGGCACATATCACTCTGTTCACTTATTAAGGGCCCCAAGGACTAGTTCCA  
440 450 460 470 480 490 500  
TGGACCAATATGAGTTCTGACCTATGCTTACCTTGCTTAACCTCACTTCTATA  
510 520 530 540 X 550 560 570  
GAACAGAAAATTCTGGCATCATAAATTGACCTGCTCATCTTACATCAAGGTTACCCAGAACCTAAGGAGT  
580 590 600 610 620 630 640  
ATTTCAGCTAAACACTGAGGATTCACACTACTAGTAACTGATGAAATTCAAAATAATG  
650 660 670 680 690 700 710 720  
CAGACTGTACACGTTCTATCAGCTGCTTCTGCTTCTGAGCAACAACTGAGGCTCTTCTG  
710 720 730 740 750 760 770 780 790

5. US-09-303-040-5 (1-1080)  
US-09-646-561-33 Sequence 33, Application US/09646561

Sequence 33, Application US/09646561

GENERAL INFORMATION:

APPLICANT: Sim, Ge-Kee

APPLICANT: Yang, Shumin

APPLICANT: Sellins, Karen S.

TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY

PROTEINS, NUCLEIC

ACID MOLECULES, AND USES THEREOF

FILE REFERENCE: IM-1-CI-PCT

CURRENT APPLICATION NUMBER: US/09/646,561

CURRENT FILING DATE: 2000-09-19

PRIOR APPLICATION NUMBER: 60/078,765

PRIOR FILING DATE: 1998-03-19

PRIOR FILING NUMBER: 09/062,597

PRIOR FILING DATE: 1998-04-17

NUMBER OF SEQ ID NOS: 65

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 33

LENGTH: 359

TYPE: DNA

ORGANISM: *Felis catus*

FEATURE:

NAME/KEY: CDS

LOCATION: (1) .. (357)

Initial Score = 227 Optimized Score = 280 Significance = -1.37  
Residue Identity = 79% Matches = 291 Mismatches = 62  
Gaps = 15 Conservative Substitutions = 0

GTTTCGTTGTTCTCGGGAAATGTCAGCTGAGCTTACATGCTGTTCTGCTGTTCTCATGA  
80 90 100 110 120 130 140  
GTGACAGCACTATTCACAGGAACTGGAAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  
150 160 170 180 190 200 210  
AGAGTCAAGGAAATTCACAGGAACTGGAAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  
220 230 240 250 260 270 280  
ATGAGCTGGTAGTTTGGCAGGACAGGATAAGCTGGTTCTTATAGATAATTGAGGAAAGAAC  
290 300 310 320 330 340 350 360  
CTCAAATGTTCATCTCAAAATAAGGGCCTGAGGACACACTGGGCCNGAGACTCCACA  
370 380 390 400 410 420 430  
ATGTTCAAGGACAGGGCACATATCACTCTGTTCACTTATTAAGGGCCCCAAGGACTAGTTCCA  
440 450 460 470 480 490 500  
TGGACCAATATGAGTTCTGACCTATGCTTACCTTGCTTAACCTCACTTCTATA  
510 520 530 540 X 550 560 570  
GAACAGAAAATTCTGGCATCATAAATTGACCTGCTCATCTTACATCAAGGTTACCCAGAACCTAAGGAGT  
580 590 600 610 620 630 640  
ATTTCAGCTAAACACTGAGGATTCACACTACTAGTAACTGATGAAATTCAAAATAATG  
650 660 670 680 690 700 710 720  
CAGACTGTACACGTTCTATCAGCTGCTTCTGAGCAACAACTGAGGCTCTTCTG  
710 720 730 740 750 760 770 780 790

290           300           310           320           330           340           350           360  
 CTCRAAATGTTCTCTCAAAATAAGGGCCGTACAGCTTGACAGGAACTGGACCTTGAGACTCCACA  
 ATGTCAGACAGTCAAGGACAGGSCACATATTAFACTGTTCATTCATTTAAAGGCCAAAGGACTAGTTCCA  
 TGCACCAAAATGAGTTCTGACCTATCAGTGCTTGCAACTTCAGTCACCTGAAATAACGAACTTCTATA  
 370           380           390           400           410           420           430  
 GAACTGAAATTGCTGACCTATCAGTGCTTGCAACTTCAGTCACCTGAAATAACGAACTTCTATA  
 440           450           460           470           480           490           500  
 GAACTGAAATTGCTGACCTATCAGTGCTTGCAACTTCAGTCACCTGAAATAACGAACTTCTATA  
 510           520           530           540           X        550           560           570  
 GAACTGAAATTGCTGACCTATCAGTGCTTGCAACTTCAGTCACCTGAAATAACGAACTTCTATA  
 580           590           600           610           620           630           640  
 ATTTTCAGCTAAACACTGAGAATTCACTACTAAGTAGTGTAGTACTGCTCATGAGAACTTCAGAAATRATGAA  
 ATTTCAGCTAAACACTGAGAATTCACTACTAAGTAGTGTAGTACTGCTCATGAGAAATRATGAA  
 650           660           670           680           690           700           710           720  
 CAGACTGTCAGCTGTTCTACAGCTTGCTTTCTAGCCCTGAAGCACACATGTCAGCTTGAGCTTCTTGAG  
 CAGACTGTCAGCTGTTCTACAGCTTGCTTTCTAGCCCTGAAGCACACATGTCAGCTTGAGCTTCTTGAG  
 730           740           750           760           770           780  
 CCCTGAAACTGGAGACAGTGGAGATGCTGCTCCCTACCTTCATATAGTGCACACCAA-GGATA-  
 CCCCTGAAACTGGAGACAGTGGAGATGCTGCTCCCTACCTTCATATAGTGCACACCAA-GGATA-  
 790           800           810           820           830           840           850  
 -AAGACCCCTGAAAGGCCCTACTTCCTCTGA-TTGGCGCTCTTGTGAACTGTTGTTTGTGAGA  
 AAGGAGAAC-AAGCACCAAGAGTACCATCAC-GTACCTGAGAGATGTGAGCCAGTGA  
 250           260           270           280           290           300           310  
 860           870           880           890           900           910           920           930  
 TGTTGTCCTTTAAACACTTAAAGGAAAGAGAGCTGGCCCTCTCATGATGTTGAGACCATCA  
 T-TRACATTGAGAC-AGCTCTGAGCAAGAGA-C-CTACAC  
 320           330           340           350           X  
 940           950           960           970           980           990           1000  
 AAAGGGAGAGAAAGAGACAAACAGCAACAGGAAGAGACATACCGTACCTGAGATCTGAG  
 1010           1020           1030           1040           1050           1060           1070  
 CCCAGTGTGTTAACATTGAGACAGCCCTCGGGGACAAATACTAGTGAAGAAATGCTGCTTGGGTGCT  
 1080  
 GACAAT



```
> O <
> O IntelliGenetics
> O <
```

## FastDB - Fast Pairwise Comparison of Sequences

Release 5.4

Results file us-09-303-510-5.res made by jdelaval on Fri 20 Dec 102 9:02:01-PST.

Query sequence being compared:US-09-303-510-5 (1-1080)

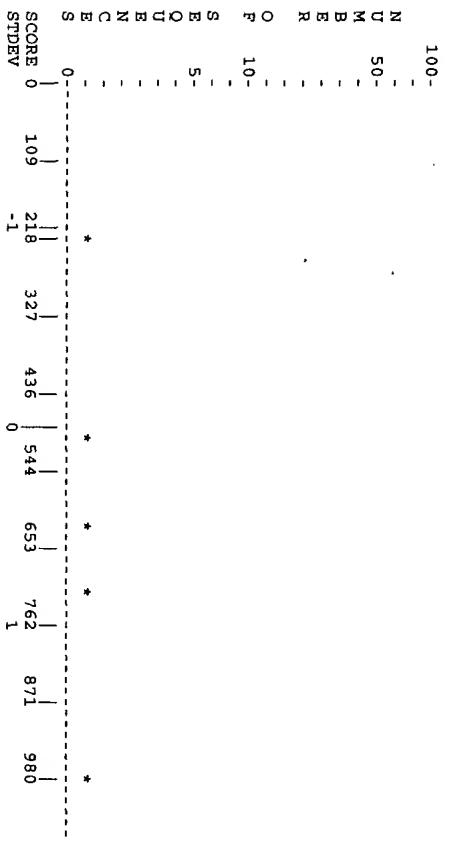
Number of sequences searched:

Number of scores above cutoff:

5

Results of the initial comparison of US-09-303-510-5 (1-1080) with:  
 File : roark-09-646561.seq

100-



## PARAMETERS

	Score:	Unitary	K-tuple	Joining Penalty	4
	Mismatch penalty	1.00	Window size	30	32
	Gap penalty	0.33			
	Cutoff score	0			
	Randomization group	0			

## SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
Times:	607	498	276.48
			Total Elapsed
			00:00:00.00

Number of residues: 3691

Number of sequences searched: 5

Number of scores above cutoff: 5

The scores below are sorted by initial score.  
 Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	***** 1 standard deviation above mean *****					
1. US-09-646-561-28	Sequence 28, Application from mean *** 0 standard deviation from mean ***	996	980	986	1.35	0
2. US-09-646-561-9	Sequence 9, Application US 987 706 868 0.36 0	987	706	868	0.36	0
3. US-09-646-561-19	Sequence 19, Application 840 625 691 0.07 0	840	625	691	0.07	0
4. US-09-646-561-30	Sequence 30, Application 509 497 501 -0.40 0	509	497	501	-0.40	0
5. US-09-646-561-33	Sequence 33, Application 359 227 280 -1.37 0	359	227	280	-1.37	0
1. US-09-303-510-5 (1-1080)	US-09-646-561-28 Sequence 28, Application US/09646561	1080	980	986	1.35	0
Sequence 28, Application US/09646561	GENERAL INFORMATION:					
APPLICANT: Sim, Ge-k Kee						
APPLICANT: Yang, Shumin						
TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY						
ACID MOLECULES, AND USES THEREOF						
FILE REFERENCE: IM-1-CL-PCT						
CURRENT APPLICATION NUMBER: US/09/646,561						
CURRENT FILING DATE: 2000-09-19						
PRIOR APPLICATION NUMBER: 60/078,765						
PRIOR FILING DATE: 1998-03-19						
PRIOR FILING DATE: 1998-04-17						
NUMBER OF SEQ ID NOS: 65						
SOFTWARE: PatentIn Ver. 2.0						
SEQ ID NO: 28						
LENGTH: 996						
TYPE: DNA						
ORGANISM: Felis catus						
Initial Score = 980	Optimized Score = 986	Significance = 1.35				
Residue Identity = 98%	Matches = 988	Mismatches = 8				
Gaps = 3	Conservative Substitutions = 0					
10	20	30	40	50	60	X
GTTCCTGTTCTGGAGAAATGCACTGAGCTTACATCAGTCCTGGCTCTGGAGGGTT						X
ATGGGATT	X					
80	90	100	110	120	130	140
GTGAGCAGCTATGGGTTGACTCACCTCGCTTGATGGCCCTCCCTCTGGGTTTCCGTA						
GTGAGCAGCTATGGGTTGACTCACCTCGCTTGATGGCCCTCCCTCTGGGTTTCCGTA						
20	30	40	50	60	70	80
150	160	170	180	190	200	210
AGAGTCAGCATATTTCACAAGACTGAGCTAACATGCCATTACAAACTCTCAAACATAAGCTGG						
AGAGTCAGCATATTTCACAAGACTGAGCTAACATGCCATTACAACTCTCAAACATAAGCTGG						
90	100	110	120	130	140	150
220	230	240	250	260	270	280
ATGAGCTCTAGTATTGGCGAGGAGTAGCTGTTGATGAGATTCAGGGCAAGAGAAC						
ATGAGCTCTAGTATTGGCGAGGAGTAGCTGTTGATGAGATTCAGGGCAAGAGAAC						
160	170	180	190	200	210	220
290	300	310	320	330	340	350
CTCAAAATGTCATCAATAAGGGCCGATCAAGCTTGTACAGGGCAACTGGACCTGAGACTCCAA						
CTCAAAATGTCATCAATAAGGGCCGATCAAGCTTGTACAGGGCAACTGGACCTGAGACTCCAA						
230	240	250	260	270	280	290
370	380	390	400	410	420	430
ATGTCATCAAGGAGCACATCTACTGTTCTCATTTATAAGGCCAAGGACTAGTC						

PRIOR FILING DATE: 1998-03-19  
 PRIOR APPLICATION NUMBER: US09/062,597  
 PRIOR FILING DATE: 1998-04-17  
 NUMBER OF SEQ ID NOS: 65  
 SOFTWARE: Patentin Ver. 2.0  
 SEQ ID NO: 9  
 LENGTH: 887  
 TYPE: DNA  
 ORGANISM: Canis familiaris

Initial Score	Optimized Score	Significance
Residue Identity	Matches	Mismatches
Gaps	Conservative Substitutions	
10	20	50
50	60	X
70		
90	110	120
120	130	140
150	160	170
180	190	200
210		
220	230	240
250	260	270
280		
300	310	320
330	340	350
360		
370	380	390
400	410	420
430		
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460	470	480
490	500	510
520	530	540
550	560	570
580	600	620
640		
660	670	680
700	710	720
730	740	750
760	780	790
790		
800	810	820
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880	890	900
910	920	930
940	950	960
970	980	990
1000		
1020	1030	1040
1050	1060	1070
1080		
1090	1100	1110
1120		
1130	1140	1150
1160		
1170	1180	1190
1200		
1210	1220	1230
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1280		
1290	1300	1310
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1330	1340	1350
1360		
1370	1380	1390
1400		
1410	1420	1430
1440		
1450	1460	1470
1480		
1490	1500	1510
1520		
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1600		
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1970	1980	1990
2000		
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2040		
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2120		
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2160		
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3160	3170	3180
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4000	4010	4020
4030		
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4080	4090	4100
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4950		
4960	4970	4980
4990		
5000	5010	5020
5030		
5040	5050	5060
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5080	5090	5100
5110		
5120	5130	5140
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5160	5170	5180
5190		
5200	5210	5220
5230		
5240	5250	5260
5270		
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5320	5330	5340
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5390		
5400	5410	5420
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5480	5490	5500
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5670		
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5870		
5880	5890	5900
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5920	5930	5940
5950		
5960	5970	5980
5990		
6000	6010	6020
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6670		
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6790		
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6990		
7000	7010	7020
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7080	7090	7100
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7200	7210	7220
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7280	7290	7300
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7390		
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7990		
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8080	8090	8100
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8200	8210	8220
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8360	8370	8380
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8400	8410	8420
843		



4. US-09-303-510-5 (1-1080)  
US-09 646-561-30 Sequence 30, Application US/09646561

Sequence 30, Application US/09646561

GENERAL INFORMATION:

APPLICANT: Sim, Kee-Kee  
APPLICANT: Yang, Shumin  
APPLICANT: Sellins, Karen S.

TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY MOLECULES, AND USES THEREOF

FILE REFERENCE: IM-1-21-PCT

CURRENT APPLICATION NUMBER: US/09 646, 561

CURRENT FILING DATE: 2000-09-19

PRIOR APPLICATION NUMBER: 60/078,765

PRIOR FILING DATE: 1998-03-19

PRIOR APPLICATION NUMBER: 09/062,597

PRIOR FILING DATE: 1998-04-17

NUMBER OF SEQ ID NOS: 65

SOFTWARE: PatentIn Ver. 2.0

SEQID NO 30

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Initial Score = 497 Optimized Score = 501 Significance = -0.40
Residue Identity = 98% Matches = 502 Mismatches = 0
Gaps = 1 Conservative Substitutions = 0

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          80   90   100  110  120  130  140
GTGAGAGCAGTATGGACTGAGTCACTCTCCTGATGGCCTCTGCTCTGCTCTGCTCTGCTCTG
          150  160  170  180  190  200  210
AGAGTCAGCATATTTCACAGAAGCTGAGAACTGCCATGCCATTACAACATCTAACATAGGCCTG
          220  230  240  250  260  270  280
ATGAGCTGGTAGTATTGGCAGGGACGGATAAGCTGGTCTGTATGAGGATTTAGAGGAAAGAGAAC
          290  300  310  320  330  340  350  36
CTCAAAATGTCATCTCAAATAAAGGGCCCTACAAAGCTTGACAAGGCAACTGGACCCCTGAGACTCCAC
          370  380  390  400  410  420  430
ATGTCAGATCAGGACAAGGGCACATATCACTGTTCAATTATAAGGGCCCAAAGGACTAGTTCCC
          440  450  460  470  480  490  500
TGCACCAAAATGAGTGTCTGACCTATCACTGGTGTCAACTCTGCAACCTGAAATAACGTAACTTCTAT
          510  520  530  540  550  560  570
GAACAGAAAATTCTGGCATATAAAATTGACCTGCTCATOTATCAAAAGTACCTGAAACCTAAGGAGATG
          610  620  630  640
          650  660  670  680  690  700  710  72
          730  740  750  760  770  780  790

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SEQ ID NO	LENGTH:	TYPE:	ORGANISM:	FEATURE:	NAME/KEY:	CDS	LOCATION:	Initial Score	Optimized Score	Score	Matches	Mismatches	Significance
1	190	DNA	Felis catus				(1)..(357)	227	227	280	291	291	-1.37
2	200	DNA	Felis catus				(1)..(357)	29%	29%	280	291	291	62
3	210	DNA	Felis catus				(1)..(357)	290	290	290	300	300	0
4	220	DNA	Felis catus				(1)..(357)	290	290	290	300	300	0
5	230	DNA	Felis catus				(1)..(357)	290	290	290	300	300	0
6	800	DNA	Felis catus				(1)..(357)	840	850	860	860	860	0
7	870	DNA	Felis catus				(1)..(357)	910	920	930	930	930	0
8	940	DNA	Felis catus				(1)..(357)	970	980	990	990	990	1000
9	1010	DNA	Felis catus				(1)..(357)	1040	1050	X	1060	1070	1080
10	1080	DNA	Felis catus				(1)..(357)	410	420	430	440	450	460
11	1150	DNA	Felis catus				(1)..(357)	480	490	500	X	X	X
12	1220	DNA	Felis catus				(1)..(357)	340	350	360	370	380	390
13	1290	DNA	Felis catus				(1)..(357)	270	280	290	300	310	0
14	1360	DNA	Felis catus				(1)..(357)	260	270	280	290	300	0
15	1430	DNA	Felis catus				(1)..(357)	250	260	270	280	290	0
16	1500	DNA	Felis catus				(1)..(357)	240	250	260	270	280	0
17	1570	DNA	Felis catus				(1)..(357)	230	240	250	260	270	0
18	1640	DNA	Felis catus				(1)..(357)	220	230	240	250	260	0
19	1710	DNA	Felis catus				(1)..(357)	210	220	230	240	250	0
20	1780	DNA	Felis catus				(1)..(357)	200	210	220	230	240	0
21	1850	DNA	Felis catus				(1)..(357)	190	200	210	220	230	0
22	1920	DNA	Felis catus				(1)..(357)	180	190	200	210	220	0
23	1990	DNA	Felis catus				(1)..(357)	170	180	190	200	210	0
24	2060	DNA	Felis catus				(1)..(357)	160	170	180	190	200	0
25	2130	DNA	Felis catus				(1)..(357)	150	160	170	180	190	0
26	2200	DNA	Felis catus				(1)..(357)	140	150	160	170	180	0
27	2270	DNA	Felis catus				(1)..(357)	130	140	150	160	170	0
28	2340	DNA	Felis catus				(1)..(357)	120	130	140	150	160	0
29	2410	DNA	Felis catus				(1)..(357)	110	120	130	140	150	0
30	2480	DNA	Felis catus				(1)..(357)	100	110	120	130	140	0
31	2550	DNA	Felis catus				(1)..(357)	90	100	110	120	130	0
32	2620	DNA	Felis catus				(1)..(357)	80	90	100	110	120	0
33	2690	DNA	Felis catus				(1)..(357)	70	80	90	100	110	0
34	2760	DNA	Felis catus				(1)..(357)	60	70	80	90	100	0
35	2830	DNA	Felis catus				(1)..(357)	50	60	70	80	90	0
36	2900	DNA	Felis catus				(1)..(357)	40	50	60	70	80	0
37	2970	DNA	Felis catus				(1)..(357)	30	40	50	60	70	0
38	3040	DNA	Felis catus				(1)..(357)	20	30	40	50	60	0
39	3110	DNA	Felis catus				(1)..(357)	10	20	30	40	50	0
40	3180	DNA	Felis catus				(1)..(357)	0	10	20	30	40	0

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AGAGTCAGGATATTCAAAAGACTGGAGAACTGCCCATTACAACTCTAACATAAACATAGGCTCG
220        230        240        250        260        270        280

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ATGTTCAGATCAAGGACACAGGGCACATATCCTACTGTTTCATTCATTATAAGGCCCCAAAGGAACTACTTCCCACCA							
440	450	460	470	480	490	500	
TGCCACCAAATGAGTTGACTTACAGTGCTTGCTAACCTGAACTGAACTCTAATA							
510	520	530	540	X 550	560	570	
GAACAGAAATTCGGCATATAATTGACCTGCTCATCTATCAGGTACCCGAGACCTAGGAGATCT							
				X 580	590	600	
				ATTTTCAGCTAACACTGACATTAACACTAATGTTAGTGTGATAGCTGATGAGAAATCTCAAAATAATGTA	610	620	630
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